



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/612,894A
Source: 1600
Date Processed by STIC: 7/3/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/612,894A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
 Wrapped Aminos
 The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 _____ Invalid Line Length
 The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 _____ Misaligned Amino
 Numbering
 The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 _____ Non-ASCII
 The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 _____ Variable Length
 Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 _____ PatentIn 2.0
 "bug"
 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 _____ Skipped Sequences
 (OLD RULES)
 Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 _____ Skipped Sequences
 (NEW RULES)
 Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 _____ Use of n's or Xaa's
 (NEW RULES)
 Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 _____ Invalid <213>
 Response
 Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 _____ Use of <220>
 Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 _____ PatentIn 2.0
 "bug"
 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 _____ Misuse of n
 n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/09/612,894A

TIME: 15:30:49

Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

3 <110> APPLICANT: Stocco, Douglas M
 4 <120> Clark, Barbara J
 6 <121> TITLE OF INVENTION: Compositions and Methods for Regulation of Steroidogenesis
 8 <130> FILE REFERENCE: 12491.49
 10 <140> CURRENT APPLICATION NUMBER: US 09/612,894A
 11 <141> CURRENT FILING DATE: 2000-07-10
 13 <160> NUMBER OF SEQ ID NOS: 19
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1466
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Other nucleic acid
 22 <400> SEQUENCE: 1

invalid response - see item 10 on error summary sheet

13 atttaccacac aggtctgttc aggaacttga aaggttcagg aagaacaacc cttgagcacc 60
 15 taccactaca gattgttcct agttaggttc aaggtgtgtg ctggaagctc ctatagacat 120
 17 atggcgaata tgaagcatt aaggcaccac gctgtgctgg ccattgggca agagctcaac 180
 19 tggacagcac tggggattc cagtccgggg tggatgggtc aagttogaag tggagctct 240
 31 ctgcttggtt ctcaacttga agcaaacctc tatagtgaac aggagctgtc ctacatccag 300
 33 cagggagagg tggctatgca gaaggccttg ggcatactca acaaccagga aggotggaag 360
 35 aagaaaagcc agcaggagaa cggggacgaa gtgctaagta agatggtgcc agatgtgggc 420
 37 aagggttttc gcttgagggt ggtggtagac cagcccatgg acagactcta tgaagaactt 480
 39 gtgacccgca tggaggccat gggagagtgg aacccaaaatg tcaaggagat caaggtcctg 540
 41 cagaggtatt gaaaagacac ggtcatcact catgagctgg ctgoggoggc agcaggcaac 600
 43 ctgctggggc ctgagactt cttgagcttg cgtgtgaccc agcgcagagg ttccaaactgt 660
 45 tggctggcag gattggccac acattctgg gagatggcgg agcagagtgg tgtcatcaga 720
 47 gcttaacag gctccactg cttgtgtgtt cttccactgg ctggaagtc ctccagact 780
 49 aaactcactt ggtgtctcag tactgacctg aagggttggc tgcgaagac aatcatcaac 840
 51 caggtcctat cgcagaccca gatagagttc gccaaaccac tgcgcaagcg cctggaagcc 900
 53 agccttgctt ctgaggccca gtgttaagga ctgtccacca cattgaactg caaatcattg 960
 55 gaactctcca caggaggtct gaaagtctgt ccattctcag ctaacagcat cgggaggggt 1020
 57 ggtactcagg agcactagg actgactggt aaaatcagga tcagcaaaat agaaatgagg 1080
 59 ctgagaataa agtttctcta gtgtctccca ctgcataget gtgaggcta aqggataadt 1140
 61 aatttgaaa cctttctctt aggtctgtat atgctgacat aaagacat agcactatc 1200
 63 aaaaagggat gctaaaggat gggacatttt gcttaccag ctccaaatgt caactactga 1260
 65 aagagtggtg caaacaaagc aaggtcttcc ctaggaaact ctgtaaaagt tctctctgt 1320
 67 aaaggtctag aaattctatg aaactactta caaagggtct ttccagagta ttccaaattt 1380
 69 tctctgagga gaattgaaac catcatttgg ccgacttccc taactaatcc atgacaataa 1440
 71 aacacataa taacaaaaa aaauu 1466

74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 234
 76 <212> TYPE: PRT
 77 <213> ORGANISM: amino acid
 79 <400> SEQUENCE: 1

same type of error

RAW SEQUENCE LISTING

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TIME: 15:30:49

Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

```

81 Met Phe Leu Ala Thr Phe Lys Leu Cys Ala Gly Ser Ser Tyr Arg His
82 1 5 10 15
83 Met Arg Asn Met Lys Gly Leu Arg His Gln Ala Val Leu Ala Ile Gly
84 20 25 30
85 Gln Glu Leu Asn Trp Arg Ala Leu Gly Asp Ser Ser Pro Gly Trp Met
86 35 40 45
87 Gly Gln Val Arg Arg Arg Ser Ser Leu Leu Gly Ser Gln Leu Glu Ala
88 50 55 60
89 Thr Leu Tyr Ser Asp Gln Glu Leu Ser Tyr Ile Gln Gln Gly Glu Val
90 65 70 75 80
101 Ala Met Gln Lys Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys
102 85 90 95
103 Lys Glu Ser Gln Gln Glu Asn Gly Asp Glu Val Leu Ser Lys Met Val
104 100 105 110
105 Pro Asp Val Gly Lys Val Phe Arg Leu Glu Val Val Val Asp Gln Pro
106 115 120 125
107 Met Asp Arg Leu Tyr Glu Glu Leu Val Asp Arg Met Glu Ala Met Gly
108 130 135 140
109 Glu Trp Asn Pro Asn Val Lys Gln Ile Lys Val Leu Gln Arg Ile Gly
110 145 150 155 160
111 Lys Asp Thr Val Ile Thr His Glu Leu Ala Ala Ala Ala Gly Asn
112 165 170 175
113 Leu Val Gly Pro Arg Asp Phe Val Ser Val Arg Cys Thr Lys Arg Arg
114 180 185 190
115 Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
116 195 200 205
117 Pro Glu Gln Ser Gly Val Ile Arg Ala Glu His Gly Pro Thr Cys Met
118 210 215 220
119 Val Leu His Pro Leu Ala Gly Ser Pro Ser Lys Thr Lys Leu Thr Trp
120 225 230 235 240
121 Leu Leu Ser Ile Asp Leu Lys Gly Trp Leu Pro Lys Thr Ile Ile Asn
122 245 250 255
123 Gln Val Leu Ser Gln Thr Gln Ile Glu Phe Ala Asn His Leu Arg Lys
124 260 265 270
125 Arg Leu Glu Ala Ser Pro Ala Ser Glu Ala Gln Cys
126 275 280
127 <10> SEQ ID NO: 3
128 <11> LENGTH: 14
129 <12> TYPE: PPT
130 <13> ORGANISM: Amino acid
131 <140> SEQUENCE: 3
132 Ala Glu His Gly Pro Thr Cys Met Val Leu His Pro Leu Ala
133 1 10
134 <10> SEQ ID NO: 4
135 <11> LENGTH: 12
136 <12> TYPE: PPT
137 <13> ORGANISM: Amino acid
138 <140> SEQUENCE: 4
139 Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys

```

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Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

```

173 1          5          10
175 <210> SEQ ID NO: 5
176 <211> LENGTH: 19
177 <212> TYPE: PRT
178 <213> ORGANISM: Amino acid
180 <400> SEQUENCE: 5
181 Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
182 1          5          10          15
183 <210> SEQ ID NO: 6
184 <211> LENGTH: 6
185 <212> TYPE: PRT
186 <213> ORGANISM: Amino acid
187 <400> SEQUENCE: 6
188 Asn Gln Glu Gly Trp Lys
189 1          5
191 <210> SEQ ID NO: 7
192 <211> LENGTH: 9
193 <212> TYPE: PRT
194 <213> ORGANISM: Amino acid
195 <400> SEQUENCE: 7
196 Ala Glu His Gly Pro Thr Cys Met Val
197 1          5
199 <210> SEQ ID NO: 8
200 <211> LENGTH: 11
201 <212> TYPE: PRT
202 <213> ORGANISM: Amino acid
203 <400> SEQUENCE: 8
204 Ile Leu Asn Asn Gln Glu Gly Trp Lys Lys Glu
205 1          5          10
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 15
209 <212> TYPE: DNA
210 <213> ORGANISM: other nucleic acid
212 <214> FEATURE:
213 <215> NAME/KEY: misc_feature
214 <216> LOCATION: (3)..(3)
215 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
216 <220> FEATURE:
217 <221> NAME/KEY: modified_base
218 <222> LOCATION: (6)..(6)
219 <223> OTHER INFORMATION: x = a or c
220 <220> FEATURE:
221 <221> NAME/KEY: modified_base
222 <222> LOCATION: (9)..(9)
223 <223> OTHER INFORMATION: y = c or t/u
224 <220> FEATURE:
225 <221> NAME/KEY: misc_feature
226 <222> LOCATION: (12)..(12)

```

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Input Set : D:\Steroidogenesis.ST25.txt

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147 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 149 <220> FEATURE:
 150 <221> NAME/KEY: misc_feature
 151 <222> LOCATION: (15)..(15)
 152 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 154 <220> FEATURE:
 155 <221> NAME/KEY: misc_feature
 156 <222> LOCATION: (13)..(13)
 157 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 159 <220> FEATURE:
 160 <221> NAME/KEY: modified_base
 161 <222> LOCATION: (21)..(21)
 162 <223> OTHER INFORMATION: y = c or t/u
 164 <400> SEQUENCE: 9

W--> 265 gcngarcayg gncnacntg yatgg

25

165 <210> SEQ ID NO: 19
 166 <211> LENGTH: 25
 167 <212> TYPE: DNA
 168 <213> ORGANISM: other nucleic acid
 169 <220> FEATURE:
 170 <221> NAME/KEY: modified_base
 171 <222> LOCATION: (5)..(5)
 172 <223> OTHER INFORMATION: r = a or g
 174 <220> FEATURE:
 175 <221> NAME/KEY: misc_feature
 176 <222> LOCATION: (2)..(2)
 178 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 184 <220> FEATURE:
 185 <221> NAME/KEY: misc_feature
 186 <222> LOCATION: (11)..(11)
 187 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 189 <220> FEATURE:
 190 <221> NAME/KEY: misc_feature
 191 <222> LOCATION: (14)..(14)
 193 <223> OTHER INFORMATION: r = (a or c or g or t/u) or (unknown or other)
 194 <220> FEATURE:
 195 <221> NAME/KEY: modified_base
 196 <222> LOCATION: (17)..(17)
 197 <223> OTHER INFORMATION: r = a or g
 199 <220> FEATURE:
 200 <221> NAME/KEY: modified_base
 201 <222> LOCATION: (19)..(20)
 202 <223> OTHER INFORMATION: y = c or t/u
 204 <220> FEATURE:
 205 <221> NAME/KEY: misc_feature
 206 <222> LOCATION: (23)..(23)
 207 <223> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 209 <400> SEQUENCE: 10

W--> 310 ccatrcangt nggncrctgy tcngc

25

RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/09/612,894A

TIME: 15:30:49

Input Set : D:\Steroidogenesis.ST25.txt

Output Set: N:\CRF4\07032003\I612894A.raw

313 <210> SEQ ID NO: 11
 314 <211> LENGTH: 17
 315 <212> TYPE: DNA
 316 <213> ORGANISM: other nucleic acid
 319 <216> FEATURE:
 320 <217> NAME/KEY: modified_base
 321 <218> LOCATION: (5)..(5)
 322 <219> OTHER INFORMATION: y = c or t/u
 324 <216> FEATURE:
 325 <217> NAME/KEY: modified_base
 326 <218> LOCATION: (6)..(6)
 327 <219> OTHER INFORMATION: r = a or g
 329 <216> FEATURE:
 330 <217> NAME/KEY: modified_base
 331 <218> LOCATION: (9)..(9)
 332 <219> OTHER INFORMATION: r = a or g
 334 <216> FEATURE:
 335 <217> NAME/KEY: misc_feature
 336 <218> LOCATION: (12)..(12)
 337 <219> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 339 <400> SEQUENCE: 11

W--> 340 aaycarcarg gntggaa

17

341 <210> SEQ ID NO: 12
 344 <211> LENGTH: 17
 345 <212> TYPE: DNA
 346 <213> ORGANISM: other nucleic acid
 349 <216> FEATURE:
 350 <217> NAME/KEY: misc_feature
 351 <218> LOCATION: (6)..(6)
 352 <219> OTHER INFORMATION: n = (a or c or g or t/u) or (unknown or other)
 354 <216> FEATURE:
 355 <217> NAME/KEY: modified_base
 356 <218> LOCATION: (9)..(9)
 357 <219> OTHER INFORMATION: y = c or t/u
 359 <216> FEATURE:
 360 <217> NAME/KEY: modified_base
 361 <218> LOCATION: (12)..(12)
 362 <219> OTHER INFORMATION: y = c or t/u
 364 <216> FEATURE:
 365 <217> NAME/KEY: modified_base
 366 <218> LOCATION: (15)..(15)
 367 <219> OTHER INFORMATION: r = a or g
 369 <400> SEQUENCE: 12

W--> 370 ttccanccyt cytgrtt

17

371 <210> SEQ ID NO: 13
 374 <211> LENGTH: 401
 375 <212> TYPE: DNA
 376 <213> ORGANISM: other nucleic acid
 378 <400> SEQUENCE: 13

Please correct
 this type of error
 in subsequent sequences

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/612,894A

DATE: 07/03/2003
TIME: 15:30:50

Input Set : D:\Steroidogenesis.ST25.txt
Output Set: N:\CRF4\07032003\I612894A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 3,12,15,18
Seq#:10; N Pos. 8,11,14,23
Seq#:11; N Pos. 12
Seq#:12; N Pos. 6